

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/699,035B  
Source: 1FW16  
Date Processed by STIC: 10/6/06

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IFW16

## RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/699,035B

TIME: 10:14:04

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4 <110> APPLICANT: BATEMAN, JOHN
5     FITZGERALD, DAVID
7 <120> TITLE OF INVENTION: A MOLECULAR MARKER
9 <130> FILE REFERENCE: 071838.0142
11 <140> CURRENT APPLICATION NUMBER: 10/699,035B
12 <141> CURRENT FILING DATE: 2003-10-31
14 <150> PRIOR APPLICATION NUMBER: PCT/AU02/00542
15 <151> PRIOR FILING DATE: 2002-05-02
17 <150> PRIOR APPLICATION NUMBER: AU PR4701/01
18 <151> PRIOR FILING DATE: 2001-05-02
20 <160> NUMBER OF SEQ ID NOS: 41
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25 <211> LENGTH: 537
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33 tcgggtgagg ctgcccagga tgcggtgcgt gcttctgccc agcgcatggg tgacacccac 240
34 actggcctgg cgctggtcta tgccaaggaa cagctgtttg ctgaagcatc aggtgccccg 300
35 ccaggggtgc ccaaagtgtc ggtgtgggtg acagatggcg gctccagcga ccctgtgggc 360
36 ccccccatgc aggagctcaa ggacctgggc gtcaccgtgt tcattgtcag caccggccga 420
37 ggcaacttcc tggagctgtc agccgctgcc tcagcccctg ccgagaagca cctgcacttt 480
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43 <213> ORGANISM: Homo sapiens
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47   1           5           10           15
49 Tyr Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro
50   20           25           30
52 Leu Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly
53   35           40           45
55 Ser Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu
56   50           55           60
58 Ala Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr
59  65           70           75           80
61 His Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu
62   85           90           95

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64 Ala Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr
65          100          105          110
67 Asp Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys
68          115          120          125
70 Asp Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe
71          130          135          140
73 Leu Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His
74 145          150          155          160
76 Phe Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly
77          165          170          175
79 Ser Ile Leu Asp
80          180
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91 agctcagcca gcgtgtcaca ctatgagttc tcaagagttc ggaatttgt ggggcagctg 180
92 gtggctacga tgtctttcgg acccggggct ctgcgtgcta gtctggtgca cgtgggcagc 240
93 cagcctcaca cagagtttac ttttgaccag tacagttcag gccaggctat acgggatgcc 300
94 atccgtgttg caccccaacg tatgggtgat accaacacag gcctggcact ggcttatgcc 360
95 aaagaacaat tgtttgctga ggaagcaggt gcccggccag gggttcccaa ggtgctggtg 420
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98 gctgcctcgg ctctgcccga gaagcaccta cactttgtgg atgtggatga tcttctatc 600
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121 Leu Ala Arg Ser Ser Ile Glu Arg Gly Ser Thr Ala Ser Asp Pro Gln
122          20          25          30
124 Gly Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr

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125          35          40          45
127 Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Thr Met
128          50          55          60
130 Ser Phe Gly Pro Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
131 65          70          75          80
133 Gln Pro His Thr Glu Phe Thr Phe Asp Gln Tyr Ser Ser Gly Gln Ala
134          85          90          95
136 Ile Arg Asp Ala Ile Arg Val Ala Pro Gln Arg Met Gly Asp Thr Asn
137          100          105          110
139 Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu Gln Leu Phe Ala Glu Glu
140          115          120          125
142 Ala Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
143          130          135          140
145 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
146 145          150          155          160
148 Leu Gly Val Thr Ile Phe Ile Val Ser Thr Gly Arg Gly Asn Leu Leu
149          165          170          175
151 Glu Leu Leu Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe
152          180          185          190
154 Val Asp Val Asp Asp Leu Pro Ile Ala Arg Glu Leu Arg Gly Ser
155          195          200          205
157 Ile Thr Asp Ala Met Gln Pro Gln Gln Leu His Ala Ser Glu Val Leu
158          210          215          220
160 Ser Ser Gly Phe Arg Leu Ser Trp Pro Pro Leu Leu Thr Ala Asp Ser
161 225          230          235          240
163 Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Gly Lys Leu Ala Thr Thr
164          245          250          255
166 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Ser Trp Thr Trp Thr Asp
167          260          265          270
169 Leu Asp Pro Asp Thr Asp Tyr Glu Val Ser Leu Leu Pro Glu Ser Asn
170          275          280          285
172 Val His Leu Leu Arg Pro Gln His Val Arg Val Arg Thr Leu Gln Glu
173          290          295          300
175 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser
176 305          310          315          320
178 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Pro Asp Ser Ala Leu Gly
179          325          330          335
181 Tyr His Val Gln Leu Gly Pro Leu Gln Gly Gly Ser Leu Glu Arg Val
182          340          345          350
184 Glu Val Pro Ala Gly Gln Asn Ser Thr Thr Val Gln Gly Leu Thr Pro
185          355          360          365
187 Cys Thr Thr Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg
188          370          375          380
190 Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr Ala Ser Gly Ala Arg Thr
191 385          390          395          400
193 Arg Ala Pro Gln Ser Met Arg Pro Glu Ala Gly Pro Arg Glu Pro
194          405          410          415
197 <210> SEQ ID NO: 5
198 <211> LENGTH: 1254

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200 <213> ORGANISM: Homo sapiens
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205 agctcagcca gcgtctctca ctacgagttc tcccgggttc gggagtttgt ggggcagctg 180
206 gtggctccac tgcccctggg caccggggcc ctgctgcca gtctggtgca cgtgggcagt 240
207 cggccataca ccgagttccc cttcggccag cacagctcgg gtgaggtctg ccaggatgcg 300
208 gtgctgtctt ctgcccagcg catgggtgac acccacactg gcctggcgct ggtctatgcc 360
209 aaggaacagc tgtttgctga agcatcaggt gcccggccag gggtgcccaa agtgctggtg 420
210 tgggtgacag atggcggctc cagcgaccct gtgggcccc ccatacagga gctcaaggac 480
211 ctgggcgtca ccgtgttcat tgtcagcacc ggccgaggca acttcctgga gctgtcagcc 540
212 gctgcctcag cccctgccga gaagcacctg cactttgtgg acgtggatga cctgcacatc 600
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214 gagatcacgt ccagcggtt ccgcctggcc tggccacccc tgcagaccgc agactcgggc 720
215 tactatgtgc tggagctggt gcccagcgcc cagccggggg ctgcaagacg ccagcagctg 780
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217 gcgctagtgc ctgagtccaa cgtgcgcctc ctgaggcccc agatcctgcg ggtgcgcacg 900
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221 acgctgcagg gcctggcgcc gggcaccgcc tacctggtga ccgtgaccgc cgccttcgcg 1140
222 tcgggccgcg agagcgcgct gtccgccaa gctgcacgc ccgacggccc gcgcccgcgc 1200
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226 <211> LENGTH: 418
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237 Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr
238 35 40 45
240 Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu
241 50 55 60
243 Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
244 65 70 75 80
246 Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala
247 85 90 95
249 Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His
250 100 105 110
252 Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala
253 115 120 125
255 Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
256 130 135 140
258 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
259 145 150 155 160

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261 Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu
262                               165                               170                               175
264 Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe
265                               180                               185                               190
267 Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser
268                               195                               200                               205
270 Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr
271                               210                               215                               220
273 Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser
274 225                               230                               235                               240
276 Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala
277                               245                               250                               255
279 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile Trp Ala Gly
280                               260                               265                               270
282 Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro Glu Ser Asn
283                               275                               280                               285
285 Val Arg Leu Leu Arg Pro Gln Ile Leu Arg Val Arg Thr Arg Pro Glu
286                               290                               295                               300
288 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser
289 305                               310                               315                               320
291 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Ser Ala Ala Ala Leu Gly
292                               325                               330                               335
294 Tyr His Val Gln Phe Gly Pro Leu Arg Gly Gly Glu Ala Gln Arg Val
295                               340                               345                               350
297 Glu Val Pro Ala Gly Arg Asn Cys Thr Thr Leu Gln Gly Leu Ala Pro
298                               355                               360                               365
300 Gly Thr Ala Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg
301                               370                               375                               380
303 Glu Ser Ala Leu Ser Ala Lys Ala Cys Thr Pro Asp Gly Pro Arg Pro
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314 <211> LENGTH: 539
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316 <213> ORGANISM: Mus musculus
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321 gtgctagtct ggtgcacgtg ggcagccagc ctcacacaga gtttactttt gaccagtaca 180
322 gttcaggcca ggctatacgg gatgccatcc gtgttgccacc ccaacgtatg ggtgatacca 240
323 acacaggcct ggcactggct tatgccaaag aacaattgtt tgctgaggaa gcaggtgccc 300
324 ggccaggggt tccaagggtg ctggtgtggg tgacagatgg tggctccagc gaccccgtag 360
325 gccccctat gcaggagctc aaggacctgg gtgtcaccat cttcattgtc agcactggcc 420
326 gaggcaacct gttggagctg ttggcagctg ctcgggctcc tgccgagaag cacctacact 480
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**VERIFICATION SUMMARY**

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PATENT APPLICATION: US/10/699,035B

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